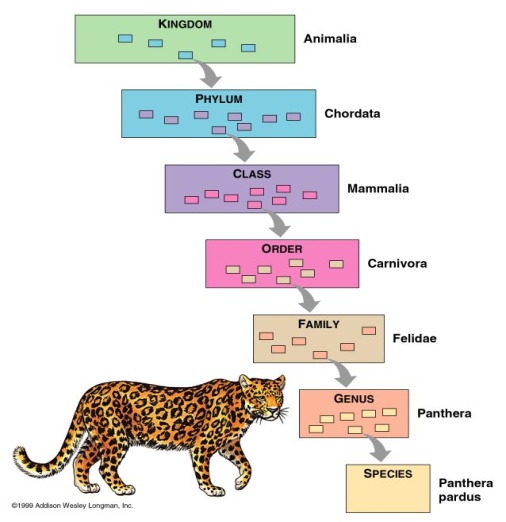
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**Unit 2 Notes, Part 2 – Classification and Biodiversity**

Ms. OK, AP Biology, 2014-2015

1. **How do scientists place organisms into groups (classify them)?**
2. Today, scientists consider phylogeny when classifying organisms. Phylogeny is defined as the evolutionary history of a species or a group of related species ; uses evidence from systematics (a scientific discipline focused on determining evolutionary relationships between organisms based on fossil, morphology/anatomy, and molecular evidence)
3. Taxonomists are scientists that use phylogeny to group organisms into categories

-The “father of modern taxonomy” was a scientist named Carolus Linnaeus

-Linnaeus created the system of binomial nomenclature, a two-part naming system that includes the “genus” name (group of similar species) and “species identifier” (ex: *Canis familiaris –* Common dog)

-Scientific names are written in Latin to ensure that names are the same anywhere in the world

Ex: Common Names for Bluegill = bream, sunperch, blue sunfish, copperbelly ; Scientific Name = *Lepomis macrochirus*

-The hierarchical classification of organisms consists of the following levels, starting with the most general/inclusive level: domain, kingdom, phylum. class, order, family, genus, and species.

1. **What evidence do scientists use to determine phylogeny?**
2. Scientists use morphological and molecular data to infer phylogeny (evolutionary history)
3. Morphological data

-Homologous structures = similarities due to shared ancestry (having a common ancestor) ; result from divergent evolution – ex: the bones of a whale’s flipper and a tiger’s paw

-Analogous structures = similarities due to similar environmental requirements and similar functions ; these similarities do not indicate shared ancestry ; result from convergent evolution – ex: the wings of a butterfly and a bat

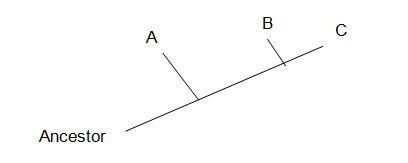
1. Molecular data

-DNA and amino acid sequences

-The more alike the DNA or amino acid sequences of two organisms, the more closely related they are evolutionarily

1. **How can we use diagrams to show evolutionary relationships between groups of organisms?**
2. A cladogram depicts patterns of shared traits (either morphological or molecular) among groups of organisms
3. Shared DERIVED traits/characters are used determine whether two groups are very closely related… these are traits that are shared among closely related groups and their RECENT COMMON ANCESTOR (meaning they are not found in a REALLY OLD COMMON ANCESTOR shown at the “root” of the cladogram… shared derived traits are also called synapomorphies
4. Why can’t we use traits from a REALLY OLD ANCESTOR to make a cladogram?

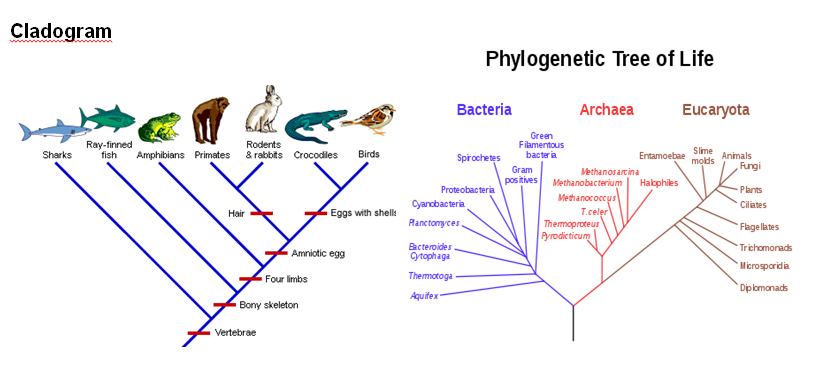
Let’s think about constructing a cladogram for a jellyfish, starfish, and humans. The basic outline of the cladogram is shown below, with the root of the diagram representing the ancestor of all three groups. Each point of branching on the cladogram is called a “node” and represents an ancestor of the species that branch off from it. The age of this ancestor can be determined based on how close it is to the root or tip of the tree. The ends of the branches represent the three current groups. First, we have to figure out which two of the three groups given are most closely related. These will be placed close together on the diagram.



The jellyfish and starfish live in the water, have radial symmetry, and are invertebrates,

so you might suppose that they belong together in a group. However, all three characteristics are believed to have been present in the common ancestor of all animals (i.e. A REALLY OLD ANCESTOR), so they can’t help determine which of these animals are most closely related. Over time, humans have simply “lost” the characteristics found in this ancestor. In reality, humans and starfish are the two groups that are most closely related. Therefore, species “A” represents jellyfish, and “B” and “C” represent starfish and humans. An example of a trait found in humans and starfish that comes from a RECENT COMMON ANCESTOR (and therefore was never found in the starfish group) is a circulatory system.

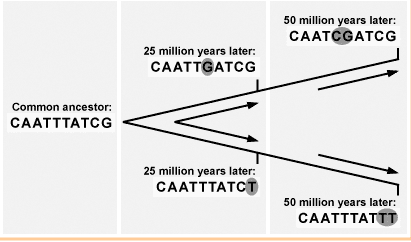
1. Phylogenetic trees are cladograms that show the relative amount of change in traits after a branching point (i.e. the length of the lines shows how much change has occurred)… *Note: Some sources will use the terms cladogram and phylogenetic tree synonymously*



1. **How can we determine the length of time that has passed since two groups “branched apart” (i.e. diverged)?**
2. The rate of evolution/change of DNA sequences varies from one part of the genetic code to another

* DNA that codes for ribosomal RNA changes relatively slowly and is useful for investigating relationships between taxa that diverged (branched off) hundreds of millions of years ago. RNA is a nucleic acid (similar to DNA) that is found in the nucleus and a cell part called a ribosome. Ribosomes are found in ALL cells (no matter what type of organism) and are used to create proteins.
* DNA found in mitochondria evolves rapidly and can be used to explore recent evolutionary events. Mitochondria are cell parts that are used to produce energy for the cell. They are one of only a couple cell parts (other than the nucleus) where DNA is found.
* Molecular clocks are sequences of DNA that seem to mutate at constant rates. For example, if a sequence tends to mutate at a rate of one base change every 25 million years and there are two bases that are different between two groups of organisms, then it is likely they branched apart 50 million years ago.

A Real Example: the gene that codes for the protein alpha-globin (a component of hemoglobin, the molecule that binds to oxygen in your red blood cells) experiences base changes at a rate of .56 changes per base pair per billion year

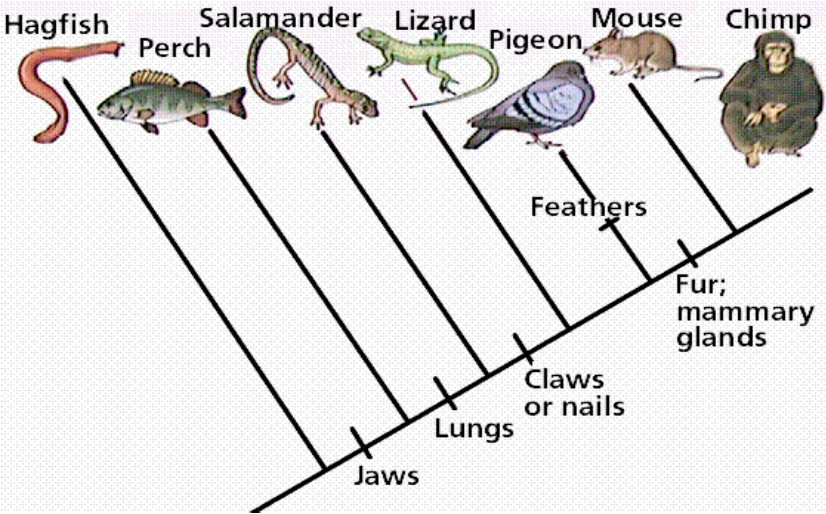


***Sequence serving as a molecular clock (one base change every 25 million years)***

**Follow-Up Questions**

***Part 1: Analyzing a Cladogram***

Analyze the cladogram below by answering the associated questions.



1. After which animals did mammary glands develop?\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

2. What animal does not have jaws? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

3. Which animals have lungs? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

4. Which animals are probably predators? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

5. After which animal did protection from the elements arise?\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

***Part 2: Creating a Cladogram***

To make a cladogram, you must first look at the animals you are studying and establish characteristics that they share and ones that are unique to each group. For the animals on the table, indicate whether the characteristic is present or not by placing a checkmark in boxes for organisms that possess a given trait. Based on that chart, create a cladogram

**Step 1: Creating a Table of Shared Characteristics**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Cells | Backbone | Legs | Hair | Opposable Thumbs |
| Slug |  |  |  |  |  |
| Catfish |  |  |  |  |  |
| Frog |  |  |  |  |  |
| Tiger |  |  |  |  |  |
| Human |  |  |  |  |  |

**Step 2: Creating a Venn Diagram** (on a separate page)

Draw a large box. Inside the box, write the name of the most general characteristic and the name of the organism that has ONLY that characteristic (Cells: Slugs). Continue creating boxes for the more specific traits using this same method. The largest box will represent the trait that is closest to the “root” of your cladogram.” The smallest box will represent the trait that is most specific (near the tip of one of your branches).

**Step 3: Draw Your Cladogram** (on a separate page)

Note: each trait will represent a “tick mark” on the tree. Again, traits that are shared by most of the organisms will be shown by tick marks that are closer to the “root” of the cladogram

1. **Do all living organisms share a common ancestor?**
2. To determine whether all organisms on Earth shared one really old ancestor, scientists decided to determine whether there were traits shared by all organisms on Earth. Below is a list of traits they found that are common to all living things and therefore provide evidence for a universal common ancestor.

-A common genetic code based on DNA

-Common processes (replication) and molecules (enzymes) used to create a copy of DNA for new cells

-Common processes (transcription and translation) and molecules (enzymes) used to create proteins from the code in DNA using 20 different protein building blocks called “amino acids”

-A common energy storage molecule called ATP and common processes of creating this molecule (cellular respiration)

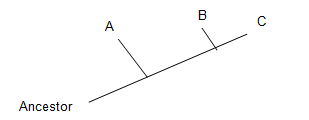
-Common cellular features (ex: a watery fluid called the cytoplasm surrounded by a membrane made of lipid / fat molecules)

1. Based on their research, scientists have also determined what the universal common ancestor might have “looked like”. They believe it was an organism similar to a modern bacterium. It probably was small and single celled. It most likely had a cell wall and a small ring of DNA at the middle of the cell. It most likely lived in harsh environments like deep ocean vents, used anaerobic respiration (a process of creating ATP without using oxygen), and was a heterotroph (i.e. could not create its own food, so it had to consume other organisms for sustenance). From the universal common ancestor, modern organisms have lost certain traits and gained certain traits to give them the characteristics they have today.
2. **Into what groups have scientists classified organisms based on their evolutionary history?**
3. Originally, scientists grouped organisms into five main kingdoms: monera, protista, fungi, plantae, and animalia based on number of cells found in the organisms, cell parts and features, method of obtaining food, habitat, and method of reproduction. Monera included all single celled organisms that lacked a nucleus (i.e., prokaryotes)
4. Upon realizing that organisms in monera were too different to be placed in one kingdom, scientists split kingdom monera into two groups, the archaebacteria and eubacteria. The five kingdom system thus became a six kingdom system.
5. Recently, a scientist named Carl Woese proposed that we look at ribosomal RNA base sequences to determine how to group organisms. Molecular sequences (i.e. DNA or RNA sequences) often provide more accurate data to determine the relationships between organisms. Based on their ribosomal RNA sequences, Woese determined that four of the kingdoms (protista, fungi, plantae, and animalia) were very closely related and thus could not be considered in separate groups, when compared to the archaebacteria and eubacteria. Therefore, he created a three domain system with kingdom archaebacteria falling into domain archaea, kingdom eubacteria falling into domain bacteria, and all four remaining kingdoms falling into domain eukarya. The characteristics distinguishing the three domains and the four kingdoms of domain eukarya are given in the chart below.

|  |  |
| --- | --- |
| **Domain or Kingdom** | **Distinguishing Features** |
| Domain Bacteria | * Prokaryotic cells (lack a nucleus and most cell parts / organelles) * Unicellular (have only one cell) * Some bacteria are heterotrophs (must eat other organisms) and some are autotrophs (can make their own food) * Tend to live in less extreme environments * *Example Organisms:* *E. coli (bacteria that live in your intestines), streptococcus (bacteria that cause strep throat), cyanobacteria (blue/green bacteria that can go through photosynthesis)* |
| Domain Archaea | * Prokaryotic cells * Unicellular * Some archaea are heterotrophs and some are autotrophs * Tend to live in extreme environments with high heat, low oxygen, and harsh chemicals (ex: deep sea vents, geysers) * *Example organisms: methanogens (archaea that create methane), thermophiles (heat loving archaea), and halophiles (salt loving archaea)* |
| Domain Eukarya | * Eukaryotic cells   -Contain a nucleus  -Contain membrane-bound cell parts / organelles (ex: mitochondria or chloroplasts)   * Some are unicellular and some are multicellular * Some eukarya are heterotrophs (ex: animals, fungi), and some are autotrophs (ex: plants) |
| Kingdom Protista | * Most are unicellular * Some are heterotrophs, some are autotrophs * Live mostly in aquatic environments * Broken down into three groups based on how they compare to the other three eukaryotic kingdoms: animal-like protists, plant-like protists, and fungus-like protists * *Example Organisms: Amoeba and Paramecium (two animal-like protists), Euglena (two plant-like protists), Volvox (a colonial protists)* |
| Kingdom Fungi | * Most are multicellular with a basic body structure made of filaments called hyphae (used for absorbing food and reproducing), some are unicellular (i.e. the yeasts) * They are heterotrophs that send out enzymes to break down food and absorb it through their hyphae (because they digest their food outside their cells this is called extracellular digestion) * Most terrestrial, some aquatic. * *Example Organisms: Yeasts, mushrooms, molds, rusts* |
| Kingdom Plantae | * All are multicellular * They are autotrophs that make their own food through a process called photosynthesis * Most terrestrial, some aquatic * *Example Organisms: Mosses, ferns, pine trees, flowering plants* |
| Kingdom Animalia | * All are multicellular * They are heterotrophs that digest their food using enzymes after bringing it into their bodies * Some are terrestrial and some are aquatic * *Example Organisms: Sponges, jellyfish, worms (flat, round, and segmented), arthropods, mollusks, starfish, and vertebrates (organisms with a backbone including fish, amphibians, reptiles, birds, and mammals)* |

**Follow-Up Questions**

1. Based on only the information in the chart above, use the cladogram below to show the relationships between the three domains (Bacteria, Archaea, and Eukarya). In other words, which two groups seem most closely related to one another?



**Answers:**

-Domain A: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

-Domain B: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

-Domain C: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1. Would you change your answers if you knew the information given below? How would you change it?

**New Information:** rRNA (ribosomal RNA) sequences between Archaea and Eukarya seem to have fewer changes than rRNA sequences between Archaea and Bacteria or Eukarya and Bacteria. Also, both Archaea and Eukarya appear to have similar DNA features that are not found in Bacteria. For example, both have their DNA wrapped around proteins called histones and possess sections of DNA called introns that are not used to code for proteins.